Amendments to the Claims

Claim 1 (currently amended): An isolated polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID ~~NOS~~ NOS: 1-34.

Claim 2 (original): A fragment of said isolated polynucleotide of claim 1, wherein said fragment comprises a polymorphic site in the polymorphic sequence.

Claim 3 (currently amended): An isolated polynucleotide comprising a sequence complementary to one or more of the polymorphic sequences ~~(SEQ ID NOS 1-34)~~ of claim 1.

Claim 4 (original): A fragment of said complementary nucleotide sequence of claim 3, wherein said fragment comprises a polymorphic site in the polymorphic sequence.

Claim 5 (currently amended): The isolated polynucleotide of claim 1 ~~any of claims 1 to 4~~, wherein said polynucleotide is selected from the group consisting of DNA, RNA, cDNA~~, or~~ and mRNA.

Claim 6 (currently amended): The isolated polynucleotide of claim 1 ~~any of claims 1 to 5~~, wherein at least one single nucleotide polymorphism is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID ~~No.~~ NO: 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 3,

position [CYP3A4_5' region -747] of SEQ ID ~~No.~~ NO: 4, position [CYP3A4_ IVS7 -202] of SEQ ID ~~No.~~ NO: 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 6, position [CYP3A4_ IVS2 -132] of SEQ ID ~~No.~~ NO: 7, position [CYP3A4_IVS1 -868] of SEQ ID ~~No.~~ NO: 8, position [CYP3A4_5' region -847] of SEQ ID ~~No.~~ NO: 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 11, position [CYP3A4_IVS3 +1992] of SEQ ID ~~No.~~ NO: 12, position [CYP3A4_IVS9 +841] of SEQ ID ~~No.~~ NO: 13, position [CYP3A4_IVS12 -473] of SEQ ID ~~No.~~ NO: 14, position [CYP3A4_IVS12 +581] of SEQ ID ~~No.~~ NO: 15, position [CYP3A4_IVS12 +586] of SEQ ID ~~No.~~ NO: 16, position [CYP3A4_IVS12 +646] of SEQ ID ~~No.~~ NO: 17, position [CYP3A4_IVS3 -734] of SEQ ID ~~No.~~ NO: 18, position [CYP17_IVS1 -271] of SEQ ID ~~No.~~ NO: 19, position [CYP17_IVS5 +75] of SEQ ID ~~No.~~ NO: 20, position [CYP17_IVS1 +426] of SEQ ID ~~No.~~ NO: 21, position [CYP17_IVS1 -99] of SEQ ID ~~No.~~ NO: 22, position [CYP17_IVS1 -700] of SEQ ID ~~No.~~ NO: 23, position [CYP17_IVS1 -565] of SEQ ID ~~No.~~ NO: 24, position [CYP17_IVS3 +141] of SEQ ID ~~No.~~ NO: 25, position [CYP17_5' region -1488] of SEQ ID ~~No.~~ NO: 26, position [CYP17_5' region -1204] of SEQ ID ~~No.~~ NO: 27, position [CYP17_IVS1 +466] of SEQ ID ~~No.~~ NO: 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 31, position [SRD5A2_5' region -870] of SEQ ID ~~No.~~ NO: 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID ~~No.~~ NO: 33 and position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 34.

Claim 7 (currently amended): The isolated polynucleotide of claim 6, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID ~~No.~~ NO: 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 3, [CYP3A4_5' region -747C>G] of SEQ ID ~~No.~~ NO: 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID ~~No.~~ NO: 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID ~~No.~~ NO: 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID ~~No.~~ NO: 7, [CYP3A4_IVS1 -868C>T] of SEQ ID ~~No.~~ NO: 8, [CYP3A4_5' region -847A>T] of SEQ ID ~~No.~~ NO: 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID ~~No.~~ NO: 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID ~~No.~~ NO: 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID ~~No.~~ NO: 12, [CYP3A4_IVS9 +841T>G] of SEQ ID ~~No.~~ NO: 13, [CYP3A4_IVS12 -473T>G] of SEQ ID ~~No.~~ NO: 14, [CYP3A4_IVS12 +581C>T] of SEQ ID ~~No.~~ NO: 15, [CYP3A4_IVS12 +586G>A] of SEQ ID ~~No.~~ NO: 16, [CYP3A4_IVS12 +646C>A] of SEQ ID ~~No.~~ NO: 17, [CYP3A4_IVS3 -734G>A] of SEQ ID ~~No.~~ NO: 18, [CYP17_IVS1 -271A>C] of SEQ ID ~~No.~~ NO: 19, [CYP17_IVS5 +75C>G] of SEQ ID ~~No.~~ NO: 20, [CYP17_IVS1 +426G>A] of SEQ ID ~~No.~~ NO: 21, [CYP17_IVS1 -99C>T] of SEQ ID ~~No.~~ NO: 22, [CYP17_IVS1 -700C>G] of SEQ ID ~~No.~~ NO: 23, [CYP17_IVS1 -565G>A] of SEQ ID ~~No.~~ NO: 24, [CYP17_IVS3 +141A>T] of SEQ ID ~~No.~~ NO: 25, [CYP17_5' region -1488C>G] of SEQ ID ~~No.~~ NO: 26, [CYP17_5' region -1204C>T] of SEQ ID ~~No.~~ NO: 27, [CYP17_IVS1 +466G>A] of SEQ ID ~~No.~~ NO: 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID ~~No.~~ NO: 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID ~~No.~~ NO: 31, [SRD5A2_5' region -870G>A] of SEQ ID ~~No.~~ NO: 32, [SRD5A2_5' region

-2036(A)7-8] of SEQ ID ~~No.~~ NO: 33 and [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID ~~No.~~ NO: 34.

Claim 8 (original): The complement of any of the isolated polynucleotides of claim 7.

Claim 9 (currently amended): The isolated polynucleotide of claim 1 ~~any of claims 1 to 8~~, wherein the nucleotide comprises part of the *CYP17* gene, the *CYP3A4* gene or the *SRD5A2* gene.

Claim 10 (currently amended): A polypeptide encoded by ~~a~~ the polynucleotide of claim 1 ~~according to any of claims 1 to 9~~.

Claim 11 (currently amended): An antibody to ~~a~~ the polypeptide ~~according to~~ of claim 10.

Claim 12 (currently amended): The isolated polynucletotide of claim 1 ~~any of claims 1 to 9~~, further comprising a detectable label.

Claim 13 (original): The isolated polynucleotide of claim 12, wherein said detectable label is selected from the group consisting of fluorophore, radionuclide, peptide, enzyme, antibody and antigen.

Claim 14 (currently amended): The isolated polynucleotide of claim 13, wherein said fluorophore is a fluorescent compound ~~is~~ selected from the group consisting of

Hoechst 33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633, DRAQ5 and Alexa 488.

Claim 15 (currently amended): A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising analysing a biological sample containing nucleic acid obtained from said subject to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID ~~No.~~ NO: 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 3, position [CYP3A4_5' region -747] of SEQ ID ~~No.~~ NO: 4, position [CYP3A4_ IVS7 -202] of SEQ ID ~~No.~~ NO: 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 6, position [CYP3A4_ IVS2 -132] of SEQ ID ~~No.~~ NO: 7, position [CYP3A4_IVS1 -868] of SEQ ID ~~No.~~ NO: 8, position [CYP3A4_5' region -847] of SEQ ID ~~No.~~ NO: 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 11, position [CYP3A4_IVS3 +1992] of SEQ ID ~~No.~~ NO: 12, position [CYP3A4_IVS9 +841] of SEQ ID ~~No.~~ NO: 13, position [CYP3A4_IVS12 -473] of SEQ ID ~~No.~~ NO: 14, position [CYP3A4_IVS12 +581] of SEQ ID ~~No.~~ NO: 15, position [CYP3A4_IVS12 +586] of SEQ ID ~~No.~~ NO: 16, position [CYP3A4_IVS12 +646] of SEQ ID ~~No.~~ NO: 17, position [CYP3A4_IVS3 -734] of SEQ ID ~~No.~~ NO: 18, position [CYP17_IVS1 -271] of SEQ ID ~~No.~~ NO: 19, position [CYP17_IVS5 +75] of SEQ ID ~~No.~~ NO: 20, position [CYP17_IVS1 +426] of SEQ ID ~~No.~~ NO: 21, position [CYP17_IVS1 -99] of SEQ ID ~~No.~~ NO: 22, position [CYP17_IVS1 -700] of SEQ ID ~~No.~~ NO: 23, position

[CYP17_IVS1 -565] of SEQ ID ~~No.~~ NO: 24, position [CYP17_IVS3 +141] of SEQ ID ~~No.~~ NO: 25, position [CYP17_5' region -1488] of SEQ ID ~~No.~~ NO: 26, position [CYP17_5' region -1204] of SEQ ID ~~No.~~ NO: 27, position [CYP17_IVS1 +466] of SEQ ID ~~No.~~ NO: 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 31, position [SRD5A2_5' region -870] of SEQ ID ~~No.~~ NO: 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID ~~No.~~ NO: 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 34, position [SRD5A2_IVS2+626] of SEQ ID ~~No.~~ NO: 35, position [SRD5A2_5' region -8029] of SEQ ID ~~No.~~ NO: 36, position [CYP3A4_IVS7+34] of SEQ ID ~~No.~~ NO: 42, position [CYP3A4_5' region –1232] of SEQ ID ~~No.~~ NO: 43, position [SRD5A2_5' region –3001] of SEQ ID ~~No.~~ NO: 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 45.

Claim 16 (currently amended): The method ~~according to~~ of claim 15, wherein said nucleic acid is selected from the group consisting of DNA, RNA, cDNA ~~or~~ and mRNA.

Claim 17 (currently amended): The method of claim 15 ~~according to claims 15 or 16~~, wherein said single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID ~~No.~~ NO: 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 3, [CYP3A4_5' region -747C>G] of SEQ ID ~~No.~~ NO: 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID ~~No.~~ NO: 5, [CYP3A4, 2204 base pairs

after the stop codon, G>C] of SEQ ID ~~No.~~ NO: 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID ~~No.~~ NO: 7, [CYP3A4_IVS1 -868C>T] of SEQ ID ~~No.~~ NO: 8, [CYP3A4_5' region -847A>T] of SEQ ID ~~No.~~ NO: 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID ~~No.~~ NO: 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID ~~No.~~ NO: 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID ~~No.~~ NO: 12, [CYP3A4_IVS9 +841T>G] of SEQ ID ~~No.~~ NO: 13, [CYP3A4_IVS12 -473T>G] of SEQ ID ~~No.~~ NO: 14, [CYP3A4_IVS12 +581C>T] of SEQ ID ~~No.~~ NO: 15, [CYP3A4_IVS12 +586G>A] of SEQ ID ~~No.~~ NO: 16, [CYP3A4_IVS12 +646C>A] of SEQ ID ~~No.~~ NO: 17, [CYP3A4_IVS3 -734G>A] of SEQ ID ~~No.~~ NO: 18, [CYP17_IVS1 -271A>C] of SEQ ID ~~No.~~ NO: 19, [CYP17_IVS5 +75C>G] of SEQ ID ~~No.~~ NO: 20, [CYP17_IVS1 +426G>A] of SEQ ID ~~No.~~ NO: 21, [CYP17_IVS1 -99C>T] of SEQ ID ~~No.~~ NO: 22, [CYP17_IVS1 -700C>G] of SEQ ID ~~No.~~ NO: 23, [CYP17_IVS1 -565G>A] of SEQ ID ~~No.~~ NO: 24, [CYP17_IVS3 +141A>T] of SEQ ID ~~No.~~ NO: 25, [CYP17_5' region -1488C>G] of SEQ ID ~~No.~~ NO: 26, [CYP17_5' region -1204C>T] of SEQ ID ~~No.~~ NO: 27, [CYP17_IVS1 +466G>A] of SEQ ID ~~No.~~ NO: 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID ~~No.~~ NO: 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID ~~No.~~ NO: 31, [SRD5A2_5' region -870G>A] of SEQ ID ~~No.~~ NO: 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID ~~No.~~ NO: 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID ~~No.~~ NO: 34, [SRD5A2_IVS2+626C>T] of SEQ ID ~~No.~~ NO: 35, [SRD5A2_5' region -8029C>T] of SEQ ID ~~No.~~ NO: 36, [CYP3A4_IVS7+ 34T>G] of SEQ ID ~~No.~~ NO: 42, [CYP3A4_5' region –1232C>T] of SEQ ID ~~No.~~ NO: 43, [SRD5A2_5' region –3001G>A] of SEQ ID ~~No.~~ NO: 44 and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 45.

Claim 18 (currently amended): The method of claim 15 ~~according to claims 15 or 16~~, wherein said single nucleotide polymorphism is selected from the complement of any of the single nucleotide polymorphisms ~~of claim 17~~.

Claim 19 (currently amended): The method of claim 15 ~~any of claims 15 to 18~~, wherein said analysis is accomplished by a process selected from the group consisting of sequencing, genotyping, fragment analysis, hybridisation, restriction fragment analysis, oligonucleotide ligation ~~or~~ and allelle specific PCR.

Claim 20 (currently amended): The method of claim 19, wherein the analysis is accomplished by hybridisation~~, the method~~ comprising the steps of

i) contacting said nucleic acid with an oligonucleotide that hybridises to one or more isolated polynucleotide polymorphic sequence selected from the group consisting of SEQ ID ~~NOS~~ NOS: 1-36 and SEQ ID ~~NOS~~ NOS: 42-45 or its complement;

ii) determining whether the nucleic acid and said oligonucleotide hybridize;

whereby hybridisation of the nucleic acid to the oligonucleotide indicates the presence of the polymorphic site in the nucleic acid.

Claim 21 (currently amended): A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, or predicting an individual's response to a drug, said method comprising adding an antibody to a polypeptide present in a biological sample obtained from said subject which polypeptide is encoded by a polynucleotide selected from the group consisting

of SEQ ID ~~NOS~~ NOS: 1-36 and SEQ ID ~~NOS~~ NOS: 42-45, or the complement thereof, and detecting specific binding of said antibody to said polypeptide.

Claim 22 (currently amended): A kit comprising at least one isolated polynucleotide of at least 5 contiguous nucleotides of SEQ ID ~~NOS~~ NOS: 1-36 or SEQ ID ~~NOS~~ NOS: 42-45, or the complement thereof, and containing at least one single nucleotide polymorphic site associated with a disease, condition or disorder related to prostate or breast cancer, together with instructions for the use thereof for detecting the presence or the absence of said at least single nucleotide polymorphism in said nucleic acid.

Claim 23 (currently amended): An oligonucleotide array comprising at least one oligonucleotide capable of hybridising to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide comprises a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID ~~NOS~~ NOS: 1-36 or SEQ ID ~~NOS~~ NOS: 42-45.

Claim 24 (currently amended): The oligonucleotide array ~~according to~~ of claim 23, wherein said first polynucleotide comprises a fragment of any of said nucleotide sequences, said fragment comprising a polymorphic site in said polymorphic sequence.

Claim 25 (currently amended): The oligonucleotide array ~~according to~~ of claim 23, wherein the first polynucleotide is a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences of SEQ ID ~~NOS~~ NOS: 1-36 or SEQ ID ~~NOS~~ NOS: 42-45.

Claim 26 (currently amended): The oligonucleotide array ~~according to~~ of claim 25, wherein the first polynucleotide comprises a fragment of said complementary sequence, said fragment comprising a polymorphic site in said polymorphic sequence.

Claim 27 (currently amended): The kit of claim 22 ~~or the array of any of claims 23 to 26~~, wherein the position of said polymorphic site is at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID ~~No.~~ NO: 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 3, position [CYP3A4_5' region -747] of SEQ ID ~~No.~~ NO: 4, position [CYP3A4_ IVS7 -202] of SEQ ID ~~No.~~ NO: 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 6, position [CYP3A4_ IVS2 -132] of SEQ ID ~~No.~~ NO: 7, position [CYP3A4_IVS1 -868] of SEQ ID ~~No.~~ NO: 8, position [CYP3A4_5' region -847] of SEQ ID ~~No.~~ NO: 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 11, position [CYP3A4_IVS3 +1992] of SEQ ID ~~No.~~ NO: 12, position [CYP3A4_IVS9 +841] of SEQ ID ~~No.~~ NO: 13, position [CYP3A4_IVS12 -473] of SEQ ID ~~No.~~ NO: 14, position [CYP3A4_IVS12 +581] of SEQ ID ~~No.~~ NO: 15, position [CYP3A4_IVS12 +586] of SEQ ID ~~No.~~ NO: 16, position [CYP3A4_IVS12 +646] of SEQ ID ~~No.~~ NO: 17, position [CYP3A4_IVS3 -734] of SEQ ID ~~No.~~ NO: 18, position [CYP17_IVS1 -271] of SEQ ID ~~No.~~ NO: 19, position [CYP17_IVS5 +75] of SEQ ID ~~No.~~ NO: 20, position [CYP17_IVS1 +426] of SEQ ID ~~No.~~ NO: 21, position [CYP17_IVS1 -99] of SEQ ID ~~No.~~ NO: 22, position [CYP17_IVS1 -700] of SEQ ID ~~No.~~ NO: 23, position [CYP17_IVS1 -565] of SEQ ID ~~No.~~ NO: 24, position

[CYP17_IVS3 +141] of SEQ ID ~~No.~~ NO: 25, position [CYP17_5' region -1488] of SEQ ID ~~No.~~ NO: 26, position [CYP17_5' region -1204] of SEQ ID ~~No.~~ NO: 27, position [CYP17_IVS1 +466] of SEQ ID ~~No.~~ NO: 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 31, position [SRD5A2_5' region -870] of SEQ ID ~~No.~~ NO: 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID ~~No.~~ NO: 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 34, position [SRD5A2_IVS2+ 626] of SEQ ID ~~No.~~ NO: 35, position [SRD5A2_5' region -8029] of SEQ ID ~~No.~~ NO: 36, position [CYP3A4_IVS7+34] of SEQ ID ~~No.~~ NO: 42, position [CYP3A4_5' region –1232] of SEQ ID ~~No.~~ NO: 43, position [SRD5A2_5' region –3001] of SEQ ID ~~No.~~ NO: 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 45.

Claim 28 (currently amended): The kit of claim 22 ~~or the array of claim 27~~, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID ~~No.~~ NO: 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 3, [CYP3A4_5' region -747C>G] of SEQ ID ~~No.~~ NO: 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID ~~No.~~ NO: 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID ~~No.~~ NO: 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID ~~No.~~ NO: 7, [CYP3A4_IVS1 -868C>T] of SEQ ID ~~No.~~ NO: 8, [CYP3A4_5' region -847A>T] of SEQ ID ~~No.~~ NO: 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID ~~No.~~ NO: 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ

ID ~~No.~~ NO: 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID ~~No.~~ NO: 12, [CYP3A4_IVS9 +841T>G] of SEQ ID ~~No.~~ NO: 13, [CYP3A4_IVS12 -473T>G] of SEQ ID ~~No.~~ NO: 14, [CYP3A4_IVS12 +581C>T] of SEQ ID ~~No.~~ NO: 15, [CYP3A4_IVS12 +586G>A] of SEQ ID ~~No.~~ NO: 16, [CYP3A4_IVS12 +646C>A] of SEQ ID ~~No.~~ NO: 17, [CYP3A4_IVS3 -734G>A] of SEQ ID ~~No.~~ NO: 18, [CYP17_IVS1 -271A>C] of SEQ ID ~~No.~~ NO: 19, [CYP17_IVS5 +75C>G] of SEQ ID ~~No.~~ NO: 20, [CYP17_IVS1 +426G>A] of SEQ ID ~~No.~~ NO: 21, [CYP17_IVS1 -99C>T] of SEQ ID ~~No.~~ NO: 22, [CYP17_IVS1 -700C>G] of SEQ ID ~~No.~~ NO: 23, [CYP17_IVS1 -565G>A] of SEQ ID ~~No.~~ NO: 24, [CYP17_IVS3 +141A>T] of SEQ ID ~~No.~~ NO: 25, [CYP17_5' region -1488C>G] of SEQ ID ~~No.~~ NO: 26, [CYP17_5' region -1204C>T] of SEQ ID ~~No.~~ NO: 27, [CYP17_IVS1 +466G>A] of SEQ ID ~~No.~~ NO: 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID ~~No.~~ NO: 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID ~~No.~~ NO: 31, [SRD5A2_5' region -870G>A] of SEQ ID ~~No.~~ NO: 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID ~~No.~~ NO: 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID ~~No.~~ NO: 34, [SRD5A2_IVS2+626C>T] of SEQ ID ~~No.~~ NO: 35, [SRD5A2_5' region -8029C>T] of SEQ ID ~~No.~~ NO: 36, [CYP3A4_IVS7 +34T>G] of SEQ ID ~~No.~~ NO: 42, [CYP3A4_5' region –1232C>T] of SEQ ID ~~No.~~ NO: 43, [SRD5A2_5' region –3001G>A] of SEQ ID ~~No.~~ NO: 44 and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 45.

Claim 29 (currently amended): The kit of claim 28 ~~or the array of claim 27~~, wherein at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms ~~of claim 28~~.

Claim 30 (currently amended): The kit of claim 22 ~~or 27 to 29 or the array of any of claims 23 to 29~~, wherein said oligonucleotide further comprises a detectable label.

Claim 31 (currently amended): The kit of claim 30 ~~or the array of claim 30~~, wherein said label is selected from the group consisting of ~~of~~ fluorophore, radionuclide, peptide, enzyme, antibody ~~or~~ and antigen.

Claim 32 (currently amended): The kit of claim 30 ~~or the array of claim 30~~, wherein said fluorophore is a fluorescent compound selected from the group consisting of Hoechst 33342, Cy2, Cy3, Cy5, CypHer, coumarin, FITC, DAPI, Alexa 633 DRAQ5 and Alexa 488.

Claim 33 (currently amended): A method of treatment or prophylaxis of a subject comprising the steps of

i) analysing a biological sample containing nucleic acid obtained from said subject to detect the presence or absence of at least one single nucleotide polymorphism in SEQ ID ~~NOS~~ NOS: 1-36 or SEQ ID ~~NOS~~ NOS: 42-45, or the complement thereof, associated with a disease, condition or disorder related to prostate or breast cancer; and

ii) treating the subject for said disease, condition or disorder if step i) detects the presence of at least one single nucleotide polymorphism in SEQ ID NOS: 1-36 or SEQ ID ~~NOS~~ NOS: 42-45, or the complement thereof.

Claim 34 (original): The method of claim 33, wherein said nucleic acid is selected from the group consisting of DNA, RNA and mRNA.

Claim 35 (currently amended): The method of claim 33 ~~claims 33 or 34~~, wherein the sample is analysed to detect the presence or absence of at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID ~~No.~~ NO: 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 3, position [CYP3A4_5' region -747] of SEQ ID ~~No.~~ NO: 4, position [CYP3A4_ IVS7 -202] of SEQ ID ~~No.~~ NO: 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 6, position [CYP3A4_ IVS2 -132] of SEQ ID ~~No.~~ NO: 7, position [CYP3A4_IVS1 -868] of SEQ ID ~~No.~~ NO: 8, position [CYP3A4_5' region -847] of SEQ ID ~~No.~~ NO: 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 11, position [CYP3A4_IVS3 +1992] of SEQ ID ~~No.~~ NO: 12, position [CYP3A4_IVS9 +841] of SEQ ID ~~No.~~ NO: 13, position [CYP3A4_IVS12 -473] of SEQ ID ~~No.~~ NO: 14, position [CYP3A4_IVS12 +581] of SEQ ID ~~No.~~ NO: 15, position [CYP3A4_IVS12 +586] of SEQ ID ~~No.~~ NO: 16, position [CYP3A4_IVS12 +646] of SEQ ID ~~No.~~ NO: 17, position [CYP3A4_IVS3 -734] of SEQ ID ~~No.~~ NO: 18, position [CYP17_IVS1 -271] of SEQ ID ~~No.~~ NO: 19, position [CYP17_IVS5 +75] of SEQ ID ~~No.~~ NO: 20, position [CYP17_IVS1 +426] of SEQ ID ~~No.~~ NO: 21, position [CYP17_IVS1 -99] of SEQ ID ~~No.~~ NO: 22, position [CYP17_IVS1 -700] of SEQ ID ~~No.~~ NO: 23, position [CYP17_IVS1 -565] of SEQ ID ~~No.~~ NO: 24, position [CYP17_IVS3 +141] of SEQ ID ~~No.~~ NO: 25, position [CYP17_5' region -1488] of SEQ ID ~~No.~~ NO: 26, position

[CYP17_5' region -1204] of SEQ ID ~~No.~~ NO: 27, position [CYP17_IVS1 +466] of SEQ ID ~~No.~~ NO: 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 31, position [SRD5A2_5' region -870] of SEQ ID ~~No.~~ NO: 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID ~~No.~~ NO: 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 34, position [SRD5A2_IVS2+626] of SEQ ID ~~No.~~ NO: 35, position [SRD5A2_5' region -8029] of SEQ ID ~~No.~~ NO: 36, position [CYP3A4_IVS7+34] of SEQ ID ~~No.~~ NO: 42, position [CYP3A4_5' region –1232] of SEQ ID ~~No.~~ NO: 43, position [SRD5A2_5' region –3001] of SEQ ID ~~No.~~ NO: 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 45.

Claim 36 (currently amended): The method of claim 35, wherein at least one single nucleotide polymorphism is selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID ~~No.~~ NO: 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 3, [CYP3A4_5' region -747C>G] of SEQ ID ~~No.~~ NO: 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID ~~No.~~ NO: 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID ~~No.~~ NO: 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID ~~No.~~ NO: 7, [CYP3A4_IVS1 -868C>T] of SEQ ID ~~No.~~ NO: 8, [CYP3A4_5' region -847A>T] of SEQ ID ~~No.~~ NO: 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID ~~No.~~ NO: 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID ~~No.~~ NO: 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID ~~No.~~ NO: 12, [CYP3A4_IVS9 +841T>G] of SEQ ID ~~No.~~ NO: 13, [CYP3A4_IVS12 -473T>G] of SEQ ID ~~No.~~ NO:

14, [CYP3A4_IVS12 +581C>T] of SEQ ID ~~No.~~ NO: 15, [CYP3A4_IVS12 +586G>A] of SEQ ID ~~No.~~ NO: 16, [CYP3A4_IVS12 +646C>A] of SEQ ID ~~No.~~ NO: 17, [CYP3A4_IVS3 -734G>A] of SEQ ID ~~No.~~ NO: 18, [CYP17_IVS1 -271A>C] of SEQ ID ~~No.~~ NO: 19, [CYP17_IVS5 +75C>G] of SEQ ID ~~No.~~ NO: 20, [CYP17_IVS1 +426G>A] of SEQ ID ~~No.~~ NO: 21, [CYP17_IVS1 -99C>T] of SEQ ID ~~No.~~ NO: 22, [CYP17_IVS1 -700C>G] of SEQ ID ~~No.~~ NO: 23, [CYP17_IVS1 -565G>A] of SEQ ID ~~No.~~ NO: 24, [CYP17_IVS3 +141A>T] of SEQ ID ~~No.~~ NO: 25, [CYP17_5' region -1488C>G] of SEQ ID ~~No.~~ NO: 26, [CYP17_5' region -1204C>T] of SEQ ID ~~No.~~ NO: 27, [CYP17_IVS1 +466G>A] of SEQ ID ~~No.~~ NO: 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID ~~No.~~ NO: 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID ~~No.~~ NO: 31, [SRD5A2_5' region -870G>A] of SEQ ID ~~No.~~ NO: 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID ~~No.~~ NO: 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID ~~No.~~ NO: 34, [SRD5A2_IVS2+626C>T] of SEQ ID ~~No.~~ NO: 35, [SRD5A2_5' region -8029C>T] of SEQ ID ~~No.~~ NO: 36, [CYP3A4_IVS7+34T>G] of SEQ ID ~~No.~~ NO: 42, [CYP3A4_5' region –1232C>T] of SEQ ID ~~No.~~ NO: 43, [SRD5A2_5' region –3001G>A] of SEQ ID ~~No.~~ NO: 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 45.

Claim 37 (currently amended): The method of claim 36 ~~35~~, wherein at least one single nucleotide polymorphism is the complement of any of the single nucleotide polymorphisms ~~of claim 36~~.

Claim 38 (currently amended): The method of claim 33 ~~any of claims 33 to 37~~, wherein said method counteracts the effect of said at least one single nucleotide polymorphism detected.

Claim 39 (currently amended): The method of claim 33 ~~claims 33 to 38~~, wherein the method comprises treatment with a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID ~~NOS~~ NOS: 1-36 and SEQ ID ~~NOS~~ NOS: 42-45, or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID ~~No.~~ NO: 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 3, position [CYP3A4_5' region -747] of SEQ ID ~~No.~~ NO: 4, position [CYP3A4_ IVS7 -202] of SEQ ID ~~No.~~ NO: 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 6, position [CYP3A4_ IVS2 -132] of SEQ ID ~~No.~~ NO: 7, position [CYP3A4_IVS1 -868] of SEQ ID ~~No.~~ NO: 8, position [CYP3A4_5' region -847] of SEQ ID ~~No.~~ NO: 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 11, position [CYP3A4_IVS3 +1992] of SEQ ID ~~No.~~ NO: 12, position [CYP3A4_IVS9 +841] of SEQ ID ~~No.~~ NO: 13, position [CYP3A4_IVS12 -473] of SEQ ID ~~No.~~ NO: 14, position [CYP3A4_IVS12 +581] of SEQ ID ~~No.~~ NO: 15, position [CYP3A4_IVS12 +586] of SEQ ID ~~No.~~ NO: 16, position [CYP3A4_IVS12 +646] of SEQ ID ~~No.~~ NO: 17, position [CYP3A4_IVS3 -734] of SEQ ID ~~No.~~ NO: 18, position [CYP17_IVS1 -271] of SEQ ID ~~No.~~ NO: 19, position [CYP17_IVS5 +75] of SEQ ID ~~No.~~ NO: 20, position [CYP17_IVS1 +426] of SEQ ID ~~No.~~ NO: 21, position

[CYP17_IVS1 -99] of SEQ ID ~~No.~~ NO: 22, position [CYP17_IVS1 -700] of SEQ ID ~~No.~~ NO: 23, position [CYP17_IVS1 -565] of SEQ ID ~~No.~~ NO: 24, position [CYP17_IVS3 +141] of SEQ ID ~~No.~~ NO: 25, position [CYP17_5' region -1488] of SEQ ID ~~No.~~ NO: 26, position [CYP17_5' region -1204] of SEQ ID ~~No.~~ NO: 27, position [CYP17_IVS1 +466] of SEQ ID ~~No.~~ NO: 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 31, position [SRD5A2_5' region -870] of SEQ ID ~~No.~~ NO: 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID ~~No.~~ NO: 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 34, position [SRD5A2_IVS2 +626] of SEQ ID ~~No.~~ NO: 35, position [SRD5A2_5' region -8029] of SEQ ID ~~No.~~ NO: 36, position [CYP3A4_IVS7+34] of SEQ ID ~~No.~~ NO: 42, position [CYP3A4_5' region –1232] of SEQ ID ~~No.~~ NO: 43, position [SRD5A2_5' region –3001] of SEQ ID ~~No.~~ NO: 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 45.

Claim 40 (currently amended): The method of claim 39, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID ~~No.~~ NO: 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 3, [CYP3A4_5' region -747C>G] of SEQ ID ~~No.~~ NO: 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID ~~No.~~ NO: 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID ~~No.~~ NO: 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID ~~No.~~ NO: 7, [CYP3A4_IVS1 -868C>T] of

SEQ ID ~~No.~~ NO: 8, [CYP3A4_5' region -847A>T] of SEQ ID ~~No.~~ NO: 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID ~~No.~~ NO: 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID ~~No.~~ NO: 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID ~~No.~~ NO: 12, [CYP3A4_IVS9 +841T>G] of SEQ ID ~~No.~~ NO: 13, [CYP3A4_IVS12 -473T>G] of SEQ ID ~~No.~~ NO: 14, [CYP3A4_IVS12 +581C>T] of SEQ ID ~~No.~~ NO: 15, [CYP3A4_IVS12 +586G>A] of SEQ ID ~~No.~~ NO: 16, [CYP3A4_IVS12 +646C>A] of SEQ ID ~~No.~~ NO: 17, [CYP3A4_IVS3 -734G>A] of SEQ ID ~~No.~~ NO: 18, [CYP17_IVS1 -271A>C] of SEQ ID ~~No.~~ NO: 19, [CYP17_IVS5 +75C>G] of SEQ ID ~~No.~~ NO: 20, [CYP17_IVS1 +426G>A] of SEQ ID ~~No.~~ NO: 21, [CYP17_IVS1 -99C>T] of SEQ ID ~~No.~~ NO: 22, [CYP17_IVS1 -700C>G] of SEQ ID ~~No.~~ NO: 23, [CYP17_IVS1 -565G>A] of SEQ ID ~~No.~~ NO: 24, [CYP17_IVS3 +141A>T] of SEQ ID ~~No.~~ NO: 25, [CYP17_5' region -1488C>G] of SEQ ID ~~No.~~ NO: 26, [CYP17_5' region -1204C>T] of SEQ ID ~~No.~~ NO: 27, [CYP17_IVS1 +466G>A] of SEQ ID ~~No.~~ NO: 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID ~~No.~~ NO: 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID ~~No.~~ NO: 31, [SRD5A2_5' region -870G>A] of SEQ ID ~~No.~~ NO: 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID ~~No.~~ NO: 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID ~~No.~~ NO: 34, [SRD5A2_IVS2+626C>T] of SEQ ID ~~No.~~ NO: 35, [SRD5A2_5' region -8029C>T] of SEQ ID ~~No.~~ NO: 36, [CYP3A4_IVS7+34T>G] of SEQ ID ~~No.~~ NO: 42, [CYP3A4_5' region –1232C>T] of SEQ ID ~~No.~~ NO: 43, [SRD5A2_5' region –3001G>A] of SEQ ID ~~No.~~ NO: 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 45.

Claim 41 (currently amended): The method of claim 40 ~~39~~, wherein the polymorphic sequence does not contain ~~at least one single nucleotide polymorphism which is~~ the complement of any of the single nucleotide polymorphisms ~~of claim 40~~.

Claim 42 (currently amended): The method of claim 33 ~~any of claims 33 to 38~~, wherein said method comprises treatment with a polypeptide which is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID ~~NOS~~ NOS: 1-36 and SEQ ID ~~NOS~~ NOS: 42-45 or their complement, provided that the polymorphic sequence, or the complement, does not contain at least one single nucleotide polymorphism at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID ~~No.~~ NO: 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 3, position [CYP3A4_5' region -747] of SEQ ID ~~No.~~ NO: 4, position [CYP3A4_ IVS7 -202] of SEQ ID ~~No.~~ NO: 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 6, position [CYP3A4_ IVS2 -132] of SEQ ID ~~No.~~ NO: 7, position [CYP3A4_IVS1 -868] of SEQ ID ~~No.~~ NO: 8, position [CYP3A4_5' region -847] of SEQ ID ~~No.~~ NO: 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 11, position [CYP3A4_IVS3 +1992] of SEQ ID ~~No.~~ NO: 12, position [CYP3A4_IVS9 +841] of SEQ ID ~~No.~~ NO: 13, position [CYP3A4_IVS12 -473] of SEQ ID ~~No.~~ NO: 14, position [CYP3A4_IVS12 +581] of SEQ ID ~~No.~~ NO: 15, position [CYP3A4_IVS12 +586] of SEQ ID ~~No.~~ NO: 16, position [CYP3A4_IVS12 +646] of SEQ ID ~~No.~~ NO: 17, position [CYP3A4_IVS3 -734] of SEQ ID ~~No.~~ NO: 18, position [CYP17_IVS1 -271] of SEQ ID ~~No.~~ NO: 19, position [CYP17_IVS5 +75] of SEQ ID ~~No.~~ NO: 20,

position [CYP17_IVS1 +426] of SEQ ID ~~No.~~ NO: 21, position [CYP17_IVS1 -99] of SEQ ID ~~No.~~ NO: 22, position [CYP17_IVS1 -700] of SEQ ID ~~No.~~ NO: 23, position [CYP17_IVS1 -565] of SEQ ID ~~No.~~ NO: 24, position [CYP17_IVS3 +141] of SEQ ID ~~No.~~ NO: 25, position [CYP17_5' region -1488] of SEQ ID ~~No.~~ NO: 26, position [CYP17_5' region -1204] of SEQ ID ~~No.~~ NO: 27, position [CYP17_IVS1 +466] of SEQ ID ~~No.~~ NO: 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 31, position [SRD5A2_5' region -870] of SEQ ID ~~No.~~ NO: 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID ~~No.~~ NO: 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 34, position [SRD5A2_IVS2+626] of SEQ ID ~~No.~~ NO: 35, position [SRD5A2_5' region -8029] of SEQ ID ~~No.~~ NO: 36, position [CYP3A4_IVS7+34] of SEQ ID ~~No.~~ NO: 42, position [CYP3A4_5' region –1232] of SEQ ID ~~No.~~ NO: 43, position [SRD5A2_5' region –3001] of SEQ ID ~~No.~~ NO: 44, and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 45.

Claim 43 (currently amended): The method of claim 42, wherein the polymorphic sequence does not contain at least one single nucleotide polymorphism selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID ~~No.~~ NO: 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 3, [CYP3A4_5' region -747C>G] of SEQ ID ~~No.~~ NO: 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID ~~No.~~ NO: 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID ~~No.~~ NO: 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID ~~No.~~ NO: 7, [CYP3A4_IVS1 -868C>T] of

SEQ ID ~~No.~~ NO: 8, [CYP3A4_5' region -847A>T] of SEQ ID ~~No.~~ NO: 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID ~~No.~~ NO: 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID ~~No.~~ NO: 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID ~~No.~~ NO: 12, [CYP3A4_IVS9 +841T>G] of SEQ ID ~~No.~~ NO: 13, [CYP3A4_IVS12 -473T>G] of SEQ ID ~~No.~~ NO: 14, [CYP3A4_IVS12 +581C>T] of SEQ ID ~~No.~~ NO: 15, [CYP3A4_IVS12 +586G>A] of SEQ ID ~~No.~~ NO: 16, [CYP3A4_IVS12 +646C>A] of SEQ ID ~~No.~~ NO: 17, [CYP3A4_IVS3 -734G>A] of SEQ ID ~~No.~~ NO: 18, [CYP17_IVS1 -271A>C] of SEQ ID ~~No.~~ NO: 19, [CYP17_IVS5 +75C>G] of SEQ ID ~~No.~~ NO: 20, [CYP17_IVS1 +426G>A] of SEQ ID ~~No.~~ NO: 21, [CYP17_IVS1 -99C>T] of SEQ ID ~~No.~~ NO: 22, [CYP17_IVS1 -700C>G] of SEQ ID ~~No.~~ NO: 23, [CYP17_IVS1 -565G>A] of SEQ ID ~~No.~~ NO: 24, [CYP17_IVS3 +141A>T] of SEQ ID ~~No.~~ NO: 25, [CYP17_5' region -1488C>G] of SEQ ID ~~No.~~ NO: 26, [CYP17_5' region -1204C>T] of SEQ ID ~~No.~~ NO: 27, [CYP17_IVS1 +466G>A] of SEQ ID ~~No.~~ NO: 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID ~~No.~~ NO: 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID ~~No.~~ NO: 31, [SRD5A2_5' region -870G>A] of SEQ ID ~~No.~~ NO: 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID ~~No.~~ NO: 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID ~~No.~~ NO: 34, [SRD5A2_IVS2+626C>T] of SEQ ID ~~No.~~ NO: 35, [SRD5A2_5' region -8029C>T] of SEQ ID ~~No.~~ NO: 36, [CYP3A4_IVS7+34T>G] of SEQ ID ~~No.~~ NO: 42, [CYP3A4_5' region –1232C>T] of SEQ ID ~~No.~~ NO: 43, [SRD5A2_5' region –3001G>A] of SEQ ID ~~No.~~ NO: 44, and [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 45.

Claim 44 (currently amended): The method of claim 43 ~~42~~, wherein the polymorphic sequence does not contain ~~at least one single nucleotide which is~~ the complement of any of the single nucleotide polymorphisms ~~of claim 43~~.

Claim 45 (currently amended): The method of claim 33 ~~claims 33 to 38~~, wherein said method comprises treatment with an antibody that binds specifically with a polypeptide encoded by a polynucleotide selected from the group consisting of SEQ ID ~~NOS~~ NOS: 1-36 and SEQ ID ~~NOS~~ NOS: 42-45, or the complement thereof.

Claim 46 (currently amended): A method for predicting the genetic ability of a subject or an organism to metabolise a chemical, said method comprising analysing a biological sample containing nucleic acid obtained from said subject or organism to detect the presence or absence of one or more single nucleotide polymorphisms at a position selected from the group consisting of position [CYP3A4_IVS9 +187] of SEQ ID ~~No.~~ NO: 1, position [CYP3A4, 1639 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 2, position [CYP3A4, 945 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 3, position [CYP3A4_5' region -747] of SEQ ID ~~No.~~ NO: 4, position [CYP3A4_ IVS7 -202] of SEQ ID ~~No.~~ NO: 5, position [CYP3A4, 2204 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 6, position [CYP3A4_ IVS2 -132] of SEQ ID ~~No.~~ NO: 7, position [CYP3A4_IVS1 -868] of SEQ ID ~~No.~~ NO: 8, position [CYP3A4_5' region -847] of SEQ ID ~~No.~~ NO: 9, position [CYP3A4, 766 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 10, position [CYP3A4, 1454 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 11, position [CYP3A4_IVS3 +1992] of SEQ ID ~~No.~~ NO: 12, position [CYP3A4_IVS9 +841] of SEQ ID ~~No.~~ NO: 13, position [CYP3A4_IVS12 -473] of SEQ ID ~~No.~~ NO: 14, position [CYP3A4_IVS12 +581] of SEQ ID ~~No.~~ NO: 15,

position [CYP3A4_IVS12 +586] of SEQ ID ~~No.~~ NO: 16, position [CYP3A4_IVS12 +646] of SEQ ID ~~No.~~ NO: 17, position [CYP3A4_IVS3 -734] of SEQ ID ~~No.~~ NO: 18, position [CYP17_IVS1 -271] of SEQ ID ~~No.~~ NO: 19, position [CYP17_IVS5 +75] of SEQ ID ~~No.~~ NO: 20, position [CYP17_IVS1 +426] of SEQ ID ~~No.~~ NO: 21, position [CYP17_IVS1 -99] of SEQ ID ~~No.~~ NO: 22, position [CYP17_IVS1 -700] of SEQ ID ~~No.~~ NO: 23, position [CYP17_IVS1 -565] of SEQ ID ~~No.~~ NO: 24, position [CYP17_IVS3 +141] of SEQ ID ~~No.~~ NO: 25, position [CYP17_5' region -1488] of SEQ ID ~~No.~~ NO: 26, position [CYP17_5' region -1204] of SEQ ID ~~No.~~ NO: 27, position [CYP17_IVS1 +466] of SEQ ID ~~No.~~ NO: 28, position [CYP17, 712 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 29, position [SRD5A2, 1356 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 30, position [SRD5A2, 849 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 31, position [SRD5A2_5' region -870] of SEQ ID ~~No.~~ NO: 32, position [SRD5A2_5' region between -2036 and -2030] of SEQ ID ~~No.~~ NO: 33, position [SRD5A2, 545 base pairs after the stop codon (3' UTR)] of SEQ ID ~~No.~~ NO: 34, position [SRD5A2_IVS2 +626] of SEQ ID ~~No.~~ NO: 35, position [SRD5A2_5' region -8029] of SEQ ID ~~No.~~ NO: 36, position [CYP3A4_IVS7+34] of SEQ ID ~~No.~~ NO: 42, position [CYP3A4_5' region –1232] of SEQ ID ~~No.~~ NO: 43, position [SRD5A2_5' region –3001] of SEQ ID ~~No.~~ NO: 44 and position [SRD5A2, 1552 base pairs after the stop codon] of SEQ ID ~~No.~~ NO: 45, wherein the presence of a polymorphism at one or more of said positions is indicative of the subject's or organism's ability or inability to metabolise said chemical.

Claim 47 (currently amended): The method of claim 46, wherein said analysis comprises detecting the presence or absence of one or more single nucleotide

polymorphisms selected from the group consisting of [CYP3A4_IVS9 +187C>G] of SEQ ID ~~No.~~ NO: 1, [CYP3A4, 1639 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 2, [CYP3A4, 945 base pairs after the stop codon, A>T] of SEQ ID ~~No.~~ NO: 3, [CYP3A4_5' region -747C>G] of SEQ ID ~~No.~~ NO: 4, [CYP3A4_ IVS7 -202C>T] of SEQ ID ~~No.~~ NO: 5, [CYP3A4, 2204 base pairs after the stop codon, G>C] of SEQ ID ~~No.~~ NO: 6, [CYP3A4_ IVS2 -132C>T] of SEQ ID ~~No.~~ NO: 7, [CYP3A4_IVS1 -868C>T] of SEQ ID ~~No.~~ NO: 8, [CYP3A4_5' region -847A>T] of SEQ ID ~~No.~~ NO: 9, [CYP3A4, 766 base pairs after the stop codon, delT] of SEQ ID ~~No.~~ NO: 10, [CYP3A4, 1454 base pairs after the stop codon, C>T] of SEQ ID ~~No.~~ NO: 11, [CYP3A4_IVS3 +1992T>C] of SEQ ID ~~No.~~ NO: 12, [CYP3A4_IVS9 +841T>G] of SEQ ID ~~No.~~ NO: 13, [CYP3A4_IVS12 -473T>G] of SEQ ID ~~No.~~ NO: 14, [CYP3A4_IVS12 +581C>T] of SEQ ID ~~No.~~ NO: 15, [CYP3A4_IVS12 +586G>A] of SEQ ID ~~No.~~ NO: 16, [CYP3A4_IVS12 +646C>A] of SEQ ID ~~No.~~ NO: 17, [CYP3A4_IVS3 -734G>A] of SEQ ID ~~No.~~ NO: 18, [CYP17_IVS1 -271A>C] of SEQ ID ~~No.~~ NO: 19, [CYP17_IVS5 +75C>G] of SEQ ID ~~No.~~ NO: 20, [CYP17_IVS1 +426G>A] of SEQ ID ~~No.~~ NO: 21, [CYP17_IVS1 -99C>T] of SEQ ID ~~No.~~ NO: 22, [CYP17_IVS1 -700C>G] of SEQ ID ~~No.~~ NO: 23, [CYP17_IVS1 -565G>A] of SEQ ID ~~No.~~ NO: 24, [CYP17_IVS3 +141A>T] of SEQ ID ~~No.~~ NO: 25, [CYP17_5' region -1488C>G] of SEQ ID ~~No.~~ NO: 26, [CYP17_5' region -1204C>T] of SEQ ID ~~No.~~ NO: 27, [CYP17_IVS1 +466G>A] of SEQ ID ~~No.~~ NO: 28, [CYP17, 712 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 29, [SRD5A2, 1356 base pairs after the stop codon (3' UTR), A>C] of SEQ ID ~~No.~~ NO: 30, [SRD5A2, 849 base pairs after the stop codon (3' UTR), A>G] of SEQ ID ~~No.~~ NO: 31, [SRD5A2_5' region -870G>A] of SEQ ID ~~No.~~ NO: 32, [SRD5A2_5' region -2036(A)7-8] of SEQ ID ~~No.~~ NO: 33, [SRD5A2, 545 base pairs after the stop codon (3' UTR), T>C] of SEQ ID

~~No.~~ NO: 34, [SRD5A2_IVS2+626C>T] of SEQ ID ~~No.~~ NO: 35, and [SRD5A2_5' region -8029C>T] of SEQ ID ~~No.~~ NO: 36, [CYP3A4_IVS7+34T>G] of SEQ ID ~~No.~~ NO: 42, [CYP3A4_5' region –1232C>T] of SEQ ID ~~No.~~ NO: 43, [SRD5A2_5' region –3001G>A] of SEQ ID ~~No.~~ NO: 44, [SRD5A2, 1552 base pairs after the stop codon, G>A] of SEQ ID ~~No.~~ NO: 45.

Claim 48 (currently amended): The method of claim 46 ~~either of claims 46 or 47~~, wherein the method further comprises predicting the response of the subject to the chemical by their ability or inability to metabolise the chemical.

Claim 49 (currently amended): The method of claim 46 ~~according to any of claims 46 to 48~~, wherein said chemical is a drug or a xenobiotic.

Claim 50 (currently amended): The method of claim 46 ~~according to any of claims 46 to 49~~, wherein said organism is selected from the group consisting of bacterium, fungus, protozoa, alga, fish, plant, insect and mammal.

Claim 51 (currently amended): A vector comprising a polynucleotide selected from the group consisting of a nucleotide sequence comprising one or more polymorphic sequences of SEQ ID ~~NOS~~ NOS: 1-36 or SEQ ID ~~NOS~~ NOS: 42-45.

Claim 52 (original): A host cell transformed with the vector of claim 51.

Claim 53 (original): The host cell of claim 52, wherein said host cell is selected from the group consisting of bacterium, fungus, protozoa, alga, fish, plant, insect and mammal.

Claim 54 (original): The host cell of claim 53, wherein said mammal cell is a human cell.

Claim 55 (currently amended): ~~Method~~ A method of metabolising a chemical using the host cell of claim 52 ~~either of claims 52 or 53~~.

Claim 56 (currently amended): ~~Method~~ A method for making a host cell resistant to a chemical, said method comprising transforming said cell with any of the polynucleotides of claim 1 ~~claims 1 to 9 or with any of the vectors of claim 51~~.

Claim 57 (original): An isolated haplotype selected from the group consisting of CYP3A4_Hap4 and SRD52_Hap3.

Claim 58 (currently amended): The isolated CYP3A4_Hap4 haplotype of ~~Claim~~ claim 57, wherein said haplotype comprises Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

Claim 59 (currently amended): The isolated SRD52_Hap3 haplotype of ~~Claim~~ claim 57, wherein said haplotype comprises Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at [SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].

Claim 60 (currently amended): A method for diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising analysing a biological sample obtained from said subject to detect the presence or absence of ~~a~~ the haplotype of claim 57 ~~as defined in any of claims 57-59~~.

Claim 61 (currently amended): A method of diagnosing a genetic susceptibility for a disease, condition or disorder related to prostate or breast cancer in a subject, said method comprising adding an antibody to a polypeptide present in a sample obtained from said subject which polypeptide is encoded by ~~a~~ the haplotype of claim 57 ~~as defined in any of claims 57-59~~, or the complement thereof, and detecting specific binding of said antibody to said polypeptide.

Claim 62 (currently amended): A method of treatment or prophylaxis of a subject comprising the steps of

i) analysing a sample of biological material containing a nucleic acid obtained from said subject to detect the presence or absence of at least one haplotype of claim 57 ~~as defined in any of claims 57-59~~, or the complement thereof,

associated with a disease, condition or disorder related to prostate or breast cancer; and

ii) treating the subject for said disease, condition or disorder if step i) detects the presence of at least one said haplotype, or the complement thereof.

Claim 63 (currently amended): The method of claim 62, wherein the method comprises treatment with a portion of ~~the~~ an isolated CYP3A4_Hap4 haplotype ~~according to claim 58~~ wherein said portion of said haplotype does not consist of at least one allele selected from the group consisting of Allele T at [CYP3A4_5' region –1232C>T], Allele C at [CYP3A4_5' region –747C>G], Allele G at [CYP3A4_5' region –392A>G], Allele G at [CYP3A4_IVS7+34T>G], Allele T at [CYP3A4_IVS7-202C>T], Allele G at [CYP3A4_stop+766T>G], Allele C at [CYP3A4_stop+1454C>T], Allele T at [CYP3A4_stop+1639A>T] and Allele C at [CYP3A4_stop+2204G>C].

Claim 64 (currently amended): The method of claim 62, wherein the method comprises treatment with a portion of ~~the~~ an isolated SRD5A2_Hap3 haplotype ~~of Claim 59~~ wherein said portion of said haplotype does not comprise of at least one allele selected from the group consisting of Allele C at [SRD5A2_5' region –8029C>T], Allele G at [SRD5A2_5' region –3001G>A], Allele G at [SRD5A2_145G>A], Allele G at [SRD5A2_265G>C], Allele T at [SRD5A2_IVS2+626C>T], Allele G at [SRD5A2_stop+1552G>A], Allele G at [SRD5A2_stop+3059G>A] and Allele G at [SRD5A2_stop+9301G>C].